

Figure 1  
Nucleotide Sequence and predicted protein for HLTG74

-88 GTTGTCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29  
 10 30 50  
 -28 CCCTGCTCTTCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGGCGTCCGCTCCACGTCT 31  
 -8 M A W L G A S L H V W 11  
 130 150 170  
 32 GGGGTTGGCTAATGCTCGGCAGCTGCCTCTGGCCAGAGCCAGCTGGATTCTGATGGCA 91  
 12 G W L M L G S C L L A R A Q L D S D G T 31  
 190 210 230  
 92 CCATCACTATAGAGGAGCAGATTGTCTTGCTGAAAGCGAAAGTACAATGTGAAGTCA 151  
 32 I T I E E Q I V L V L K A K V Q C E L N 51  
 250 270 290  
 152 ACATCACAGCTCAACTCCAGGAGGGAGAAGGTAATTGTTTCCCTGAATGGGATGGACTCA 211  
 52 I T A Q L Q E G E G N C F P E W D G L I 71  
 310 330 350  
 212 TTTGTTGGCCAGAGGAACAGTGGGGAATATCGGCTGTTCCATGCCCTCCTTATATT 271  
 72 C W P R G T V G K I S A V P C P P Y I Y 91  
 370 390 410  
 272 ATGACTTCAACCATAAAGGAGTGTCTTCCGACACTGTAACCCCAATGGAACATGGGATT 331  
 92 D F N H K G V A F R H C N P N G T W D F 111  
 430 450 470  
 332 TTATGCACAGCTTAAATAAAACATGGGCCAATTATTCAGACTGCCTTCGCTTCTGCAGC 391  
 112 M H S L N K T W A N Y S D C L R F L Q P 131  
 490 510 530  
 392 CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCTCTATGTAATGTATACCGTTG 451  
 132 D I S I G K Q E F C E R L Y V M Y T V G 151  
 550 570 590  
 452 GCTACTCATCTCTTTTGGTTCCTTGGCTGTGGCTATTCTCATCATTGGTTACTTCAGAC 511  
 152 Y S I S F G S L A V A I L I I G Y F R R 171  
 610 630 650  
 512 GATTGCATTGCACTAGGAACTATATCCACATGCACCTATTGTGTCTTTCATGCTGAGAG 571  
 172 L H C T R N Y I H M H L F V S F M L R A 191  
 670 690 710  
 572 CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG 631  
 192 T S I F V K D R V V H A H I G V K E L E 211

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FIGURE 1

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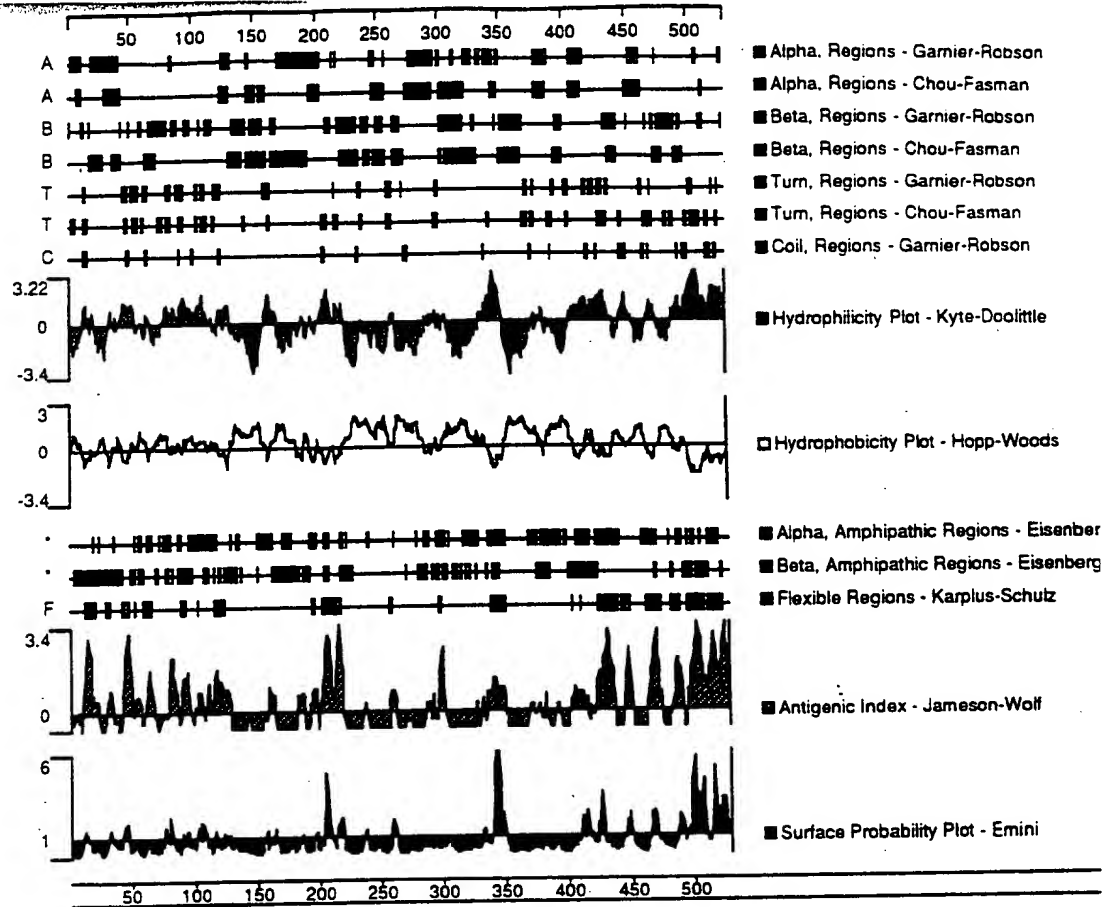
1. The first step is to identify the problem. In this case, the problem is that the company is not meeting its sales targets.

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FIGURE 1. 2/3





005270 0519200

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FIGURE 2 1/1

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PRINT OF DRAWINGS  
AS ORIGINALLY FILE

Segment Pairs: Read High Probability  
Frame Score P(N)

Segment Pairs	Read	High Probability	Frame	Score	P(N)
gp M74445 OPOPTH_1	parathyroid hormone receptor [Di...	+3	597	8.2e-204	6
pir S A39286	parathyroid hormone / parathyroi...	+3	597	2.9e-203	6
gp L04308 HUMPTH_1	parathyroid hormone receptor [Ho...	+3	580	6.7e-190	6
pir S S29610	parathyroid hormone receptor - h...	+3	580	6.1e-189	6
gp M77184 RATPATHYR_1	parathyroid hormone receptor [Ra...	+3	576	7.7e-188	6
gp X78936 MMPHRPP_1	parathyroid hormone/parathyroid ...	+3	576	7.7e-188	6
pir S A42698	parathyroid hormone and parathyr...	+3	576	7.7e-188	6
gp L34611 MUSPTHRO6_1	parathyroid hormone/parathyroid ...	+3	576	4.1e-174	6
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ...	+3	319	1.2e-96	6
gp M86835 RATVASREC_1	vasoactive intestinal polypeptid...	+3	254	3.1e-91	6

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTH\_1 parathyroid hormone receptor [Didelphis virginiana]  
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Query: 729 IMQDDPQNSIEATSVDKSYIGCKIAVVMFIYFLATNYWILVEGLYLNLIFFVAFFSDT 908  
I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLNLIFFVAFFSDT 908  
Sbjct: 253 ITEEELRAFTPEPPADKAGFVGCRVAVTVFLYFLTTNYWILVEGLYLNLIFFMAFFSEK 312

Query: 909 KYLWGFILIGWGFPAAFVAWAVARATLADARCWELSGDIKWYQAPILAAIGLNFI 1088  
KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFI 1088  
Sbjct: 313 KYLWGFILFGWGLPAFVAVVTVRATLANTECWDLSSGNKKWIIQVPIAAIVNFILF 372

Query: 1089 LNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVVLVFGVHYIVFVCLPHS 1244  
+N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++ 1244  
Sbjct: 373 INIIRVLATKLRETNAGRCDTROQYRKLKSTLVLMPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTW 446  
+G C PEWD ++CWP G GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ + N+TW 446  
Sbjct: 102 DGFCLPEWDNIVCWPAFVPGKVVAVPCPDYIYDFNHKGGRAYRRCDSNGSWELVPGNNRTW 161

Query: 447 ANYSDCLRFL 476  
ANYS+C++FL 476  
Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCEERLYVMYTVGYSSISFGLAVAILIIGYFRRLHCTRNYYIHMHLFVSFMLRATSIFV 677  
++E +RL ++YTVGYSSIS GSL VA+LI+GYFRRLHCTRNYYIHMHLFVSFMLRA SIF+ 677  
Sbjct: 177 EREVFDRLGMIYTVGYSSISLGLTAVLILGYFRRLHCTRNYYIHMHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESIMQD 740  
KD V+++ + E+E + ++ 740  
Sbjct: 237 KDAVLYSGVSTDEIERITEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNFNSFQGFVSIIYCYCNGEVQAEVKRMWSRWNLSDWKRTPPCGS 1424

FIGURE 3 1/2 325800-458

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GFFV+IIYC+CNGEVQAE+KK W L++D+KF GS  
 GFFVAIIYCF CNGEVQAEIKKSW LALDFK RKARSGS 425

Query: 1508 ISGKAAKIASRQPD SHITLPGYV 1576  
+S + A A + H LPGYV  
Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

[illegible]

FIGURE 3 2/2 325800-458